A-n● Baker

1632 #10
4/21/99
amβ

INPUT SET: S31553.raw

**This Raw Listing contains the General
Information Section and up to the first 5 pages.**

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 1                                    SEQUENCE LISTING
 2
 3    (1)     General Information:
 4          (i) APPLICANT: Susan DYMECKI
 5         (ii) TITLE OF INVENTION: Use of Flp Recombinase in Mice
 6        (iii) NUMBER OF SEQUENCES: 23
 7         (iv) CORRESPONDENCE ADDRESS:
 8              (A) ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
 9              (B) STREET: 1100 New York Avenue, N.W.
10              (C) CITY: Washington
11              (D) STATE: D.C.
12              (E) COUNTRY: USA
13              (F) ZIP: 20005-3918
14          (v) COMPUTER READABLE FORM:
15              (A) MEDIUM TYPE: Floppy disk
16              (B) COMPUTER: IBM PC compatible
17              (C) OPERATING SYSTEM: PC-DOS/MS-DOS
18              (D) SOFTWARE: Microsoft Word
19         (vi) CURRENT APPLICATION DATA:
20              (A) APPLICATION NUMBER: US 08/866,279
21              (B) FILING DATE: 30-MAY-1997
22              (C) CLASSIFICATION:
23
24    (2) INFORMATION FOR SEQ ID NO:1:
25          (i) SEQUENCE CHARACTERISTICS:
26              (A) LENGTH: 79 base pairs
27              (B) TYPE: nucleic acid
28              (C) STRANDEDNESS: single
29              (D) TOPOLOGY: linear
30         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
31    CCGGTGAAGT TCCTATTCCG AAGTTCCTAT TCTCTAGAAA GTATAGGAAC          50
32    TTCCCTAGGA GATCTTCGAA GGCTCGAGC                                 79
33
34    (2) INFORMATION FOR SEQ ID NO:2:
35          (i) SEQUENCE CHARACTERISTICS:
36              (A) LENGTH: 59 base pairs
37              (B) TYPE: nucleic acid
38              (C) STRANDEDNESS: single
39              (D) TOPOLOGY: linear
40         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
41    TAGCTACGTA GAAGTTCCTA TTCCGAAGTT CCTATTCTCT AGAAAGTATA          50
42    GGAACTTCA                                                      59
43
44    (2) INFORMATION FOR SEQ ID NO:3:
45          (i) SEQUENCE CHARACTERISTICS:
46              (A) LENGTH: 54 base pairs
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47            (B) TYPE: nucleic acid
48            (C) STRANDEDNESS: single
49            (D) TOPOLOGY: linear
50    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
51    CTAGGGAAGT TCCTATACTT TCTAGAGAAT AGGAACTTCG GAATAGGAAC          50
52    TTCA                                                           54
53
54    (2) INFORMATION FOR SEQ ID NO:4:
55         (i) SEQUENCE CHARACTERISTICS:
56            (A) LENGTH: 84 base pairs
57            (B) TYPE: nucleic acid
58            (C) STRANDEDNESS: single
59            (D) TOPOLOGY: linear
60    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
61    CCGGTGAAGT TCCTATACTT TCTAGAGAAT AGGAACTTCG GAATAGGAAC          50
62    TTCTACGTAG CTAGCTCGAG CCTTCGAAGA TCTC                           84
63
64    (2) INFORMATION FOR SEQ ID NO:5:
65         (i) SEQUENCE CHARACTERISTICS:
66            (A) LENGTH: 23 base pairs
67            (B) TYPE: nucleic acid
68            (C) STRANDEDNESS: single
69            (D) TOPOLOGY: linear
70        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
71    GTAAGGTACC GGTGAAGTTC CTA                                       23
72
73    (2) INFORMATION FOR SEQ ID NO:6:
74         (i) SEQUENCE CHARACTERISTICS:
75            (A) LENGTH: 23 base pairs
76            (B) TYPE: nucleic acid
77            (C) STRANDEDNESS: single
78            (D) TOPOLOGY: linear
79        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
80    TTCACCCACC GGTGAAGTTC CTA                                       23
81
82    (2) INFORMATION FOR SEQ ID NO:7:
83         (i) SEQUENCE CHARACTERISTICS:
84            (A) LENGTH: 211 base pairs
85            (B) TYPE: nucleic acid
86            (C) STRANDEDNESS: single
87            (D) TOPOLOGY: linear
88    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
89    GGTACCGAGC TCAGCCACCA TGACTGCTCC AAAGAAGAAG CGTAAGGTAC          50
90    CGGTGAAGTT CCTATTCCGA AGTTCCTATT CTCTAGAAAG TATAGGAACT         100
91    TCACCGGTGG GTGAAGACCA GAAACAGCAC CTCGAACTGA GCCGCGATAT         150
92    TGCCCAGCGT TTCAACGCGC TGTATGGCGA GATCGATCCC GTCGTTTTAC         200
93    AACGTCGTGA C                                                   211
94
95    (2) INFORMATION FOR SEQ ID NO:8:
96         (i) SEQUENCE CHARACTERISTICS:
97            (A) LENGTH: 64 amino acids
98            (B) TYPE: amino acid
99            (C) STRANDEDNESS: single
```

RAW SEQUENCE LISTING
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100              (D) TOPOLOGY: linear
101  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
102  Met Thr Ala Pro Lys Lys Lys Arg Lys Val Pro Val Lys Phe Leu
103  1               5               10              15
104  Phe Arg Ser Ser Tyr Ser Leu Glu Ser Ile Gly Thr Ser Pro Val
105                  20              25              30
106  Gly Glu Asp Gln Lys Gln His Leu Glu Leu Ser Arg Asp Ile Ala
107                  35              40              45
108  Gln Arg Phe Asn Ala Leu Tyr Gly Glu Ile Asp Pro Val Val Leu
109                  50              55              60
110  Gln Arg Arg Asp
111
112  (2) INFORMATION FOR SEQ ID NO:9:
113       (i) SEQUENCE CHARACTERISTICS:
114              (A) LENGTH: 8 amino acids
115              (B) TYPE: amino acid
116              (C) STRANDEDNESS: single
117              (D) TOPOLOGY: linear
118  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
119  Ala Pro Lys Lys Lys Arg Lys Val
120  1               5
121
122  (2) INFORMATION FOR SEQ ID NO:10:
123       (i) SEQUENCE CHARACTERISTICS:
124              (A) LENGTH: 16 amino acids
125              (B) TYPE: amino acid
126              (C) STRANDEDNESS: single
127              (D) TOPOLOGY: linear
128  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
129  Lys Phe Leu Phe Arg Ser Ser Tyr Ser Leu Glu Ser Ile Gly Thr
130  1               5               10              15
131  Ser
132
133  (2) INFORMATION FOR SEQ ID NO:11:
134       (i) SEQUENCE CHARACTERISTICS:
135              (A) LENGTH: 27 amino acids
136              (B) TYPE: amino acid
137              (C) STRANDEDNESS: single
138              (D) TOPOLOGY: linear
139  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
140  Pro Val Gly Glu Asp Gln Lys Gln His Leu Glu Leu Ser Arg Asp
141  1               5               10              15
142  Ile Ala Gln Arg Phe Asn Ala Leu Tyr Gly Glu Ile
143                  20              25
144
145  (2) INFORMATION FOR SEQ ID NO:12:
146       (i) SEQUENCE CHARACTERISTICS:
147              (A) LENGTH: 13 base pairs
148              (B) TYPE: nucleic acid
149              (C) STRANDEDNESS: single
150              (D) TOPOLOGY: linear
151  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
152  GAAGTTCCTA TTC                                        13
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153
154    (2) INFORMATION FOR SEQ ID NO:13:
155         (i) SEQUENCE CHARACTERISTICS:
156             (A) LENGTH: 13 base pairs
157             (B) TYPE: nucleic acid
158             (C) STRANDEDNESS: single
159             (D) TOPOLOGY: linear
160    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
161    GAAGTTCCTA TAC                                             13
162
163    (2) INFORMATION FOR SEQ ID NO:14:
164         (i) SEQUENCE CHARACTERISTICS:
165             (A) LENGTH: 34 base pairs
166             (B) TYPE: nucleic acid
167             (C) STRANDEDNESS: single
168             (D) TOPOLOGY: linear
169    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
170    GAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTTC                      34
171
172    (2) INFORMATION FOR SEQ ID NO:15:
173         (i) SEQUENCE CHARACTERISTICS:
174             (A) LENGTH: 48 base pairs
175             (B) TYPE: nucleic acid
176             (C) STRANDEDNESS: single
177             (D) TOPOLOGY: linear
178    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
179    GAAGTTCCTA TTCCGAAGTT CCTATTCTCT AGAAAGTATA GGAACTTC       48
180
181    (2) INFORMATION FOR SEQ ID NO:16:
182         (i) SEQUENCE CHARACTERISTICS:
183             (A) LENGTH: 1272 base pairs
184             (B) TYPE: nucleic acid
185             (C) STRANDEDNESS: single
186             (D) TOPOLOGY: linear
187    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
188    ATGCCACAAT TTGATATATT ATGTAAAACA CCACCTAAGG TGCTTGTTCG TCAGTTTGTG    60
189    GAAAGGTTTG AAAGACCTTC AGGTGAGAAA ATAGCATTAT GTGCTGCTGA ACTAACCTAT   120
190    TTATGTTGGA TGATTACACA TAACGGAACA GCAATCAAGA GAGCCACATT CATGAGCTAT   180
191    AATACTATCA TAAGCAATTC GCTGAGTTTG GATATTGTCA ACAAGTCACT GCAGTTTAAA   240
192    TACAAGACGC AAAAAGCAAC AATTCTGGAA GCCTCATTAA AGAAATTGAT TCCTGCTTGG   300
193    GAATTTACAA TTATTCCTTA CTATGGACAA AAACATCAAT CTGATATCAC TGATATTGTA   360
194    AGTAGTTTGC AATTACAGTT CGAATCATCG GAAGAAGCAG ATAAGGGAAA TAGCCACAGT   420
195    AAAAAAATGC TTAAAGCACT TCTAAGTGAG GGTGAAAGCA TCTGGGAGAT CACTGAGAAA   480
196    ATACTAAATT CGTTTGAGTA TACTTCGAGA TTTACAAAAA CAAAAACTTT ATACCAATTC   540
197    CTCTTCCTAG CTACTTTCAT CAATTGTGGA AGATTCAGCG ATATTAAGAA CGTTGATCCG   600
198    AAATCATTTA AATTAGTCCA AAATAAGTAT CTGGGAGTAA TAATCCAGTG TTTAGTGACA   660
199    GAGACAAAGA CAAGCGTTAG TAGGCACATA TACTTCTTTA GCGCAAGGGG TAGGATCGAT   720
200    CCACTTGTAT ATTTGGATGA ATTTTTGAGG AATTCTGAAC CAGTCCTAAA ACGAGTAAAT   780
201    AGGACCGGCA ATTCTTCAAG CAACAAGCAG GAATACCAAT TATTAAAAGA TAACTTAGTC   840
202    AGATCGTACA ACAAAGCTTT GAAGAAAAAT GCGCCTTATT CAATCTTTGC TATAAAAAAT   900
203    GGCCCAAAAT CTCACATTGG AAGACATTTG ATGACCTCAT TTCTTTCAAT GAAGGGCCTA   960
204    ACGGAGTTGA CTAATGTTGT GGGAAATTGG AGCGATAAGC GTGCTTCTGC CGTGGCCAGG  1020
205    ACAACGTATA CTCATCAGAT AACAGCAATA CCTGATCACT ACTTCGCACT AGTTTCTCGG  1080
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206   TACTATGCAT ATGATCCAAT ATCAAAGGAA ATGATAGCAT TGAAGGATGA GACTAATCCA 1140
207   ATTGAGGAGT GGCAGCATAT AGAACAGCTA AAGGGTAGTG CTGAAGGAAG CATACGATAC 1200
208   CCCGCATGGA ATGGGATAAT ATCACAGGAG GTACTAGACT ACCTTTCATC CTACATAAAT 1260
209   AGACGCATAT AA                                                    1272
210
211   (2) INFORMATION FOR SEQ ID NO:17:
212        (i) SEQUENCE CHARACTERISTICS:
213            (A) LENGTH: 423 amino acids
214            (B) TYPE: amino acid
215            (C) STRANDEDNESS: single
216            (D) TOPOLOGY: linear
217   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
218   Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu
219   1               5                  10                 15
220   Val Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys
221                  20                 25                 30
222   Ile Ala Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile
223                  35                 40                 45
224   Thr His Asn Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr
225                  50                 55                 60
226   Asn Thr Ile Ile Ser Asn Ser Leu Ser Leu Asp Ile Val Asn Lys
227                  65                 70                 75
228   Ser Leu Gln Phe Lys Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu
229                  80                 85                 90
230   Ala Ser Leu Lys Lys Leu Ile Pro Ala Trp Glu Phe Thr Ile Ile
231                  95                 100                105
232   Pro Tyr Tyr Gly Gln Lys His Gln Ser Asp Ile Thr Asp Ile Val
233                  110                115                120
234   Ser Ser Leu Gln Leu Gln Phe Glu Ser Ser Glu Glu Ala Asp Lys
235                  125                130                135
236   Gly Asn Ser His Ser Lys Lys Met Leu Lys Ala Leu Leu Ser Glu
237                  140                145                150
238   Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys Ile Leu Asn Ser Phe
239                  155                160                165
240   Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr Leu Tyr Gln Phe
241                  170                175                180
242   Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe Ser Asp Ile
243                  185                190                195
244   Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn Lys Tyr
245                  200                205                210
246   Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr Ser
247                  215                220                225
248   Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
249                  230                235                240
250   Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val
251                  245                250                255
252   Leu Lys Arg Val Asn Arg Thr Gln Asn Ser Ser Ser Asn Lys Gln
253                  260                265                270
254   Glu Tyr Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys
255                  275                280                285
256   Ala Leu Lys Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn
257                  290                295                300
258   Gly Pro Lys Ser His Ile Gly Arg His Leu Met Thr Ser Phe Leu
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/866,279A*

INPUT SET: S31553.raw

Line   Error   Original Text